On page 38, after line 5, please insert the following two paragraphs:

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Fig. P
Figure P shows a way to measure the replication capacity of patient-derived recombinant viruses.

Fig. Q
Figure Q shows a way to measure the replication capacity of patient-derived recombinant viruses.

Please replace pages 154 and 155 with new pages 154 and 155 annexed hereto as **Exhibit A**.

In the Claims

Please amend claims 98, 101-107, 109-112, 114, 116, 117 and 121 as follows:

98. (Amended) A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a biological sample from the HIV-infected patient; and

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(b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71,

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64, 93, 23, 58, and 36, the presence of such protease-encoding nucleic acid in the patient's sample indicating a change in the patient's susceptibility to a protease inhibitor.

101 (Amended) The method of claim 100, wherein the nucleic acid has a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 84, 48, 23, 73, 53, 33, 74, 20, 90, 32, and 39 or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 66, 84, 54, 48, 33, 73, 20, 71, 64, and 93, wherein the protease inhibitor is saquinavir.

102 (Amended) The method of claim 101, wherein the nucleic acid has a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 84, 48, 23, 73, 53, 33, 74, 20, and 90, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 66, 84, 54, 48, 33, 73, 20, and 71, wherein the change in the patient's susceptibility to a protease inhibitor is indicated by a decrease in susceptibility to saquinavir.

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103 (Amended) The method of claim 101, wherein the nucleic acid has a mutation at codon 82 and a secondary mutation at codons 32 or 39, or a mutation at codon 90 and a secondary mutation at codons 64 or 93, wherein the change in the patient's susceptibility to a protease inhibitor is indicated by an increase in susceptibility to saquinavir.

104 (Amended) The method of claim 100, wherein the nucleic acid has a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, 74, wherein the protease inhibitor is indinavir.

105 (Amended) The method of claim 104, wherein the nucleic acid has a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, and 46, wherein the change in the patient's susceptibility to a protease inhibitor is indicated by a decrease in susceptibility to indinavir.

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106 (Amended) The method of claim 104, wherein the nucleic acid has a mutation at codon 90 and a secondary mutation at codons 13 or 74, wherein the change in the patient's susceptibility to a protease inhibitor is indicated by an increase in susceptibility to indinavir.

107 (Amended) The method of claim 100, wherein the nucleic acid has a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 23, 84, 53, 74, 60, 33, 36, 35, 32, and 46 or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 95, 55, 54, 82, 85, 84, 20, 72, 62, 74, 53, 48, 23, 58, 36, 64, 77, and 93.

109 (Amended) The method of claim 108, wherein the change in the patient's susceptibility to a protease inhibitor is greater than 10 fold.

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110 (Amended) The method of claim 108, wherein the nucleic acid has a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 48, 23, 84, 53, 74, 20, 60, 33, 36, 35, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 84, 53, 48, 23, 58, 20, 36, and 54, wherein the change in the patient's susceptibility to a protease inhibitor is indicated by a decrease in susceptibility to saquinavir.

111 (Amended) The method of claim 108, wherein the nucleic acid has a mutation at codon 82 and a secondary mutation at codons 32 or 46, or a mutation at codon 90 and a secondary mutation at codons 64, 77, or 93, wherein the change in the patient's susceptibility to a protease inhibitor is indicated by an increase in susceptibility to saquinavir.

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112 (Amended) The method of claim 108, wherein the nucleic acid has a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, and 90, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 95, 55, 54, 82, 85, 84, 20, 72, and 62, wherein the change in the patient's susceptibility to a protease inhibitor is indicated by a decrease in susceptibility to indinavir.

114 (Amended) A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

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(a) collecting a biological sample from the HIV-

infected patient; and

(b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and secondary mutations of at lease three codons; the presence of such protease encoding nucleic acid in the patient's sample indicating a change in the patient's susceptibility to a protease inhibitor.

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116 (Amended) The method of claim 114, wherein the secondary mutation is selected from the group consisting of codons 10, 20, 52, 53, 54, 66, 71, 73, and 84.

117 A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a biological sample from the HIV-infected patient; and

(b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 33, 23, 84, 32, 53, 90, 37, 71, 10, 54, 61, 11, and 46, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 89, 53, 84, 33, 92, 95, 54, 58, 46, 82, 36, 10, 62, 74, 15, 47, 66, 32, 55, 53, 13, and 69, the presence of such protease-encoding nucleic acid in the patient's sample indicating a change in the patient's susceptibility to a protease inhibitor.

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